

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Goddard et al. Attorney's Docket No: 39780-2630P1C4

Serial No: 09/978,191 Group Art Unit: 1646

Filed: October 15, 2001 Examiner: O'Hara, Eileen B.

For: **SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME**

Commissioner for Patents
P.O. Box 1450
Alexandria, Virginia 22313-1450

DECLARATION OF AUDREY GODDARD, Ph.D.,
PAUL J. GODOWSKI, Ph.D., AUSTIN GURNEY, Ph.D., MARGARET A. ROY
and WILLIAM I. WOOD, Ph.D. UNDER 37 CFR 1.131

We, Audrey Goddard, Ph.D., Paul J. Godowski, Ph.D., Austin Gurney, Ph.D., Margaret Roy and William I. Wood, Ph.D. do hereby declare and say as follows:

1. We are the inventors of the above-identified application.
2. We have read and understood the claims pending in this application, and are aware that the claims have been rejected as anticipated by Holtzman *et al.*, U.S. Published Patent Application 20020028508, with effective priority date April 23, 1998 (09/065,363), and Sheppard *et al.*, U.S. Published Patent Application 20030166907, with effective priority date June 18, 1997 (09/050,143)
3. The polypeptide comprising the amino acid sequence of residues 35-273 of SEQ ID NO:506 and the nucleic acid sequence of nucleotides 603-1220 of SEQ ID NO:505 in the above-identified application in the United States were sequenced and cloned prior to June 18, 1997.
4. At the time the above polypeptide was cloned and sequenced, one of the inventors, Austin Gurney, was responsible for overseeing the cloning of cDNAs which encoded novel polypeptides, including the cDNA encoding the polypeptide comprising the amino acid sequence of residues 35-273 of SEQ ID NO:506.

5. At the time the above polypeptide was cloned and sequenced, one of the inventors, Audrey Goddard, was responsible for overseeing the sequencing of nucleotides encoding novel polypeptides, including the polypeptide having the amino acid sequence of residues 35-273 of SEQ ID NO: 506 in the above-identified application.
6. At the time the nucleotide encoding the above polypeptide was cloned and sequenced, one of the inventors, William I. Wood, was responsible for overseeing the homology searches for novel polypeptides, including that for the polypeptide having the amino acid sequence of residues 35-273 of SEQ ID NO: 506 in the above-identified application.
7. The PRO213 polypeptide shown in SEQ ID NO:2 is encoded by a cDNA sequence referred to as DNA30943-1163 and shown in Figure 2 of the above-identified application.
8. A cDNA sequence DNA30943-1163 is identified as SEQ ID NO:1 and shown in Figure 1 of the above-identified application.
9. The PRO213 nucleic acid sequence was found to contain sequence errors. Therefore, the PRO213 nucleic acid sequence was resequenced and designated as 213-1 nucleic acid sequence and the translated polypeptide was designated as the PRO213-1 polypeptide.
10. The PRO213-1 polypeptide shown in SEQ ID NO:506 is encoded by a cDNA sequence referred to as DNA30943-1-1163-1 and shown in Figure 213 of the above-identified application..
11. A cDNA sequence DNA30943-1-1163-1 is identified as SEQ ID NO:505 and shown in Figure 212 of the above-identified application.
12. Copies of the pages from the GSeqEdit database and GenenGenes database which report the cloning, sequencing and functional data for the PRO213 and PRO213-1 polypeptide sequences, including its homology to human gas6, as well as the cloning, and sequencing data for the nucleic acid sequence encoding the PRO213 and PRO213-1 polypeptides are attached to this declaration (with the dates redacted) as Exhibit A.

13. The GSeqEdit report shows the full-length nucleic acid sequence for DNA30943-1-1163-1 and the full-length PRO213-1 polypeptide encoded by DNA30943-1-1163-1. The full-length nucleic acid sequence for PRO213-1 (DNA30943-1-1163-1) shown in the report includes the sequence corrections made to PRO213 (DNA30943-1163) indicated below the sequence, for example, as seen on page 5 of the report. The full-length nucleic acid sequence for PRO213 (DNA30943-1163) is the sequence shown in the GSeqEdit report without the indicated corrections.
14. The amino acid sequence of residues 1-49 of PRO213 is shown in GSeqEdit report on pages 4-5. The amino acid sequence of PRO213-1 shown in GSeqEdit report starts on page 4 and continues onto the following pages. On page 5, the top sequence is the PRO213 polypeptide sequence and the bottom sequence is the PRO213-1 polypeptide sequence.
15. The amino acid sequence starting on page 6 of the GSeqEdit is identical for both the PRO213 and PRO213-1 polypeptides. Amino acid residue number 35, shown on page 6 of the GSeqEdit report, indicates the continuous numbering of PRO213-1 polypeptide sequence from the previous page. The first amino acid on page 6 corresponds to amino acid 57 of the PRO213 polypeptide.
16. The amino acid sequence of residues 35-273 of SEQ ID NO:506 shown in Figure 213 of the above-identified application is 239 amino acids long, and is identical to the amino acid sequence of residues 57-295 of SEQ ID NO:2 shown in Figure 2 of the above-identified application.
17. The nucleic acid sequence encoding residues 35-273 of SEQ ID NO: 506 comprises residues 501-1220 of SEQ ID NO:505 in Figure 212 of the above-identified application. The nucleic acid sequence comprising residues 501-1220 of SEQ ID NO:505 is 720 nucleotides long and it includes a stop codon.
18. The portion of the PRO213 polypeptide, which is identical to the portion of the PRO213-1 polypeptide encoded by the nucleic acid sequence comprising residues 501-1220 of SEQ ID NO:505, is significantly homologous with the human growth arrest-specific 6 (gas6) protein.

19. Both DNA30943-1163 cDNA sequence and the PRO213 polypeptide encoded by DNA30943-1163 were obtained prior to June 18, 1997. Furthermore, the homology of PRO213 to human gas6 was obtained prior to June 18, 1997.
20. The DNA sequence of nucleotides 606 to 1223 of SEQ ID NO:1 is identical to nucleotides 603 to 1220 of DNA30943-1-1163-1 sequence shown in the GSeqEdit report. Further, the DNA sequences of nucleotides 606 to 1223 of SEQ ID NO:1 and nucleotides 603 to 1220 of DNA30943-1-1163-1 shown in the GSeqEdit report are identical to that of nucleotides 603-1220 of SEQ ID NO:505 disclosed in the above-identified application.
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22. The amino acid residues in the GSeqEdit report which correspond to residues 35 to 273 of SEQ ID NO: 506 are shown starting on page 6 (indicated by an arrow) to page 12 of the report.
23. Exhibit A clearly shows that amino acids residues 35 to 273 of SEQ ID NO: 506 and the nucleic acid residues 603-1220 of SEQ ID NO: 505 disclosed in the above-identified application, as well as the homology of the polypeptide to human gas6, were obtained prior to June 18, 1997.

24. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.



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5/8/05

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Paul J. Godowski, Ph.D.

Date

Austin Gurney, Ph.D.

Date

Margaret A. Roy

Date

William I. Wood, Ph.D.

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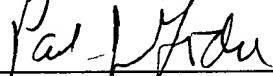
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22. The amino acid residues in the GSeqEdit report which correspond to residues 35 to 273 of SEQ ID NO: 506 are shown starting on page 6 (indicated by an arrow) to page 12 of the report.
23. Exhibit A clearly shows that amino acids residues 35 to 273 of SEQ ID NO: 506 and the nucleic acid residues 603-1220 of SEQ ID NO: 505 disclosed in the above-identified application, as well as the homology of the polypeptide to human gas6, were obtained prior to June 18, 1997.

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Paul J. Godowski, Ph.D.

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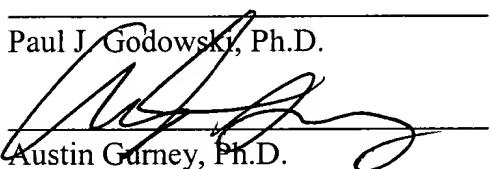
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19. Both DNA30943-1163 cDNA sequence and the PRO213 polypeptide encoded by DNA30943-1163 were obtained prior to June 18, 1997. Furthermore, the homology of PRO213 to human gas6 was obtained prior to June 18, 1997.
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21. The beginning of the cDNA sequence corresponding to nucleotides 501-1220 of SEQ ID NO:505 in the above-identified application is shown on page 6 of the GSeqEdit database report. The location of nucleotide 501 of SEQ ID:505, which corresponds to nucleotide 501 of DNA30943-1-1163-1 shown in the GSeqEdit report, is marked with an arrow. The location of nucleotide 603 of SEQ ID:505, which corresponds to nucleotide 603 of DNA30943-1-1163-1 shown on page 7 of the GSeqEdit report, is marked with an arrow. The location of the nucleotide 1220 of SEQ ID NO:505, which corresponds to nucleotide 1220 of DNA30943-1-1163-1 shown on page 12 of the GSeqEdit report, is marked with an arrow.
22. The amino acid residues in the GSeqEdit report which correspond to residues 35 to 273 of SEQ ID NO: 506 are shown starting on page 6 (indicated by an arrow) to page 12 of the report.
23. Exhibit A clearly shows that amino acids residues 35 to 273 of SEQ ID NO: 506 and the nucleic acid residues 603-1220 of SEQ ID NO: 505 disclosed in the above-identified application, as well as the homology of the polypeptide to human gas6, were obtained prior to June 18, 1997.

24. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

Audrey Goddard, Ph.D.

Date

Paul J. Godowski, Ph.D.

Date

Austin Gurney, Ph.D.

Date

Margaret A. Roy

Date



3 May 2005

William I. Wood, Ph.D.

Date

SV 2094833 v1
5/1/05 2:23 PM (39780.2630)



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Goddard et al. Attorney's Docket No: 39780-2630P1C4
Serial No: 09/978,191 Group Art Unit: 1646
Filed: October 15, 2001 Examiner: O'Hara, Eileen B.
For: **SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME**

Commissioner for Patents
P.O. Box 1450
Alexandria, Virginia 22313-1450

DECLARATION OF AUDREY GODDARD, Ph.D.,
PAUL J. GODOWSKI, Ph.D., AUSTIN GURNEY, Ph.D., MARGARET A. ROY
and WILLIAM I. WOOD, Ph.D. UNDER 37 CFR 1.131

We, Audrey Goddard, Ph.D., Paul J. Godowski, Ph.D., Austin Gurney, Ph.D., Margaret Roy and William I. Wood, Ph.D. do hereby declare and say as follows:

1. We are the inventors of the above-identified application.
2. We have read and understood the claims pending in this application, and are aware that the claims have been rejected as anticipated by Holtzman *et al.*, U.S. Published Patent Application 20020028508, with effective priority date April 23, 1998 (09/065,363), and Sheppard *et al.*, U.S. Published Patent Application 20030166907, with effective priority date June 18, 1997 (09/050,143)
3. The polypeptide comprising the amino acid sequence of residues 35-273 of SEQ ID NO:506 and the nucleic acid sequence of nucleotides 603-1220 of SEQ ID NO:505 in the above-identified application in the United States were sequenced and cloned prior to June 18, 1997.
4. At the time the above polypeptide was cloned and sequenced, one of the inventors, Austin Gurney, was responsible for overseeing the cloning of cDNAs which encoded novel polypeptides, including the cDNA encoding the polypeptide comprising the amino acid sequence of residues 35-273 of SEQ ID NO:506.

5. At the time the above polypeptide was cloned and sequenced, one of the inventors, Audrey Goddard, was responsible for overseeing the sequencing of nucleotides encoding novel polypeptides, including the polypeptide having the amino acid sequence of residues 35-273 of SEQ ID NO: 506 in the above-identified application.
6. At the time the nucleotide encoding the above polypeptide was cloned and sequenced, one of the inventors, William I. Wood, was responsible for overseeing the homology searches for novel polypeptides, including that for the polypeptide having the amino acid sequence of residues 35-273 of SEQ ID NO: 506 in the above-identified application.
7. The PRO213 polypeptide shown in SEQ ID NO:2 is encoded by a cDNA sequence referred to as DNA30943-1163 and shown in Figure 2 of the above-identified application.
8. A cDNA sequence DNA30943-1163 is identified as SEQ ID NO:1 and shown in Figure 1 of the above-identified application.
9. The PRO213 nucleic acid sequence was found to contain sequence errors. Therefore, the PRO213 nucleic acid sequence was resequenced and designated as 213-1 nucleic acid sequence and the translated polypeptide was designated as the PRO213-1 polypeptide.
10. The PRO213-1 polypeptide shown in SEQ ID NO:506 is encoded by a cDNA sequence referred to as DNA30943-1-1163-1 and shown in Figure 213 of the above-identified application..
11. A cDNA sequence DNA30943-1-1163-1 is identified as SEQ ID NO:505 and shown in Figure 212 of the above-identified application.
12. Copies of the pages from the GSeqEdit database and GenenGenes database which report the cloning, sequencing and functional data for the PRO213 and PRO213-1 polypeptide sequences, including its homology to human gas6, as well as the cloning, and sequencing data for the nucleic acid sequence encoding the PRO213 and PRO213-1 polypeptides are attached to this declaration (with the dates redacted) as Exhibit A.

13. The GSeqEdit report shows the full-length nucleic acid sequence for DNA30943-1-1163-1 and the full-length PRO213-1 polypeptide encoded by DNA30943-1-1163-1. The full-length nucleic acid sequence for PRO213-1 (DNA30943-1-1163-1) shown in the report includes the sequence corrections made to PRO213 (DNA30943-1163) indicated below the sequence, for example, as seen on page 5 of the report. The full-length nucleic acid sequence for PRO213 (DNA30943-1163) is the sequence shown in the GSeqEdit report without the indicated corrections.
14. The amino acid sequence of residues 1-49 of PRO213 is shown in GSeqEdit report on pages 4-5. The amino acid sequence of PRO213-1 shown in GSeqEdit report starts on page 4 and continues onto the following pages. On page 5, the top sequence is the PRO213 polypeptide sequence and the bottom sequence is the PRO213-1 polypeptide sequence.
15. The amino acid sequence starting on page 6 of the GSeqEdit is identical for both the PRO213 and PRO213-1 polypeptides. Amino acid residue number 35, shown on page 6 of the GSeqEdit report, indicates the continuous numbering of PRO213-1 polypeptide sequence from the previous page. The first amino acid on page 6 corresponds to amino acid 57 of the PRO213 polypeptide.
16. The amino acid sequence of residues 35-273 of SEQ ID NO:506 shown in Figure 213 of the above-identified application is 239 amino acids long, and is identical to the amino acid sequence of residues 57-295 of SEQ ID NO:2 shown in Figure 2 of the above-identified application.
17. The nucleic acid sequence encoding residues 35-273 of SEQ ID NO: 506 comprises residues 501-1220 of SEQ ID NO:505 in Figure 212 of the above-identified application. The nucleic acid sequence comprising residues 501-1220 of SEQ ID NO:505 is 720 nucleotides long and it includes a stop codon.
18. The portion of the PRO213 polypeptide, which is identical to the portion of the PRO213-1 polypeptide encoded by the nucleic acid sequence comprising residues 501-1220 of SEQ ID NO:505, is significantly homologous with the human growth arrest-specific 6 (gas6) protein.

19. Both DNA30943-1163 cDNA sequence and the PRO213 polypeptide encoded by DNA30943-1163 were obtained prior to June 18, 1997. Furthermore, the homology of PRO213 to human gas6 was obtained prior to June 18, 1997.
20. The DNA sequence of nucleotides 606 to 1223 of SEQ ID NO:1 is identical to nucleotides 603 to 1220 of DNA30943-1-1163-1 sequence shown in the GSeqEdit report. Further, the DNA sequences of nucleotides 606 to 1223 of SEQ ID NO:1 and nucleotides 603 to 1220 of DNA30943-1-1163-1 shown in the GSeqEdit report are identical to that of nucleotides 603-1220 of SEQ ID NO:505 disclosed in the above-identified application.
21. The beginning of the cDNA sequence corresponding to nucleotides 501-1220 of SEQ ID NO:505 in the above-identified application is shown on page 6 of the GSeqEdit database report. The location of nucleotide 501 of SEQ ID:505, which corresponds to nucleotide 501 of DNA30943-1-1163-1 shown in the GSeqEdit report, is marked with an arrow. The location of nucleotide 603 of SEQ ID:505, which corresponds to nucleotide 603 of DNA30943-1-1163-1 shown on page 7 of the GSeqEdit report, is marked with an arrow. The location of the nucleotide 1220 of SEQ ID NO:505, which corresponds to nucleotide 1220 of DNA30943-1-1163-1 shown on page 12 of the GSeqEdit report, is marked with an arrow.
22. The amino acid residues in the GSeqEdit report which correspond to residues 35 to 273 of SEQ ID NO: 506 are shown starting on page 6 (indicated by an arrow) to page 12 of the report.
23. Exhibit A clearly shows that amino acids residues 35 to 273 of SEQ ID NO: 506 and the nucleic acid residues 603-1220 of SEQ ID NO: 505 disclosed in the above-identified application, as well as the homology of the polypeptide to human gas6, were obtained prior to June 18, 1997.

24. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

Audrey Goddard, Ph.D.

Date

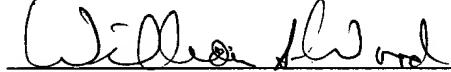
Paul J. Godowski, Ph.D.

Date

Austin Gurney, Ph.D.

Date

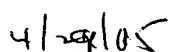
Margaret A. Roy



Date

William I. Wood, Ph.D.

Date



SV 2094833 v1
4/29/05 10:13 AM (39780.2630)

>Wednesday, [REDACTED]
>DNA30943 [Full]
>077 Sites 'A' Sites!
>[REDACTED] : DNA30943, Jean
> no stop in front

scrFI[M.hpaII-]
ncII
mspI
hpaII mspI
smaI dpmII[dam-]
scrFI[M.hpaII-]
bskI mbol/ndelI[dam-]
xbaI/psaI maeI
smaI dpmII[dam-]
scrFI[M.hpaII-]
ncII dpmI[dam+]
dsav nlaIV xbaI sau3AI taqI
tsp509I[M.ecoRI-] bfaI mbol/ndelI[dam-]
ecoRI bssKI bstYI/xholI dpmII[dam-]
dsvI[dam-]
apoI bsajI baktI hpy188III mnlI
bstNI mnlI
bskI[dam-] hpyCH4V clal/bsp106 avai[M.hpaII-] alwI[dam-]
apI[dam+] bsGI bsAJI taqI mluI ecII cac8I bsgI
bspDI[dam-] bsAJI alwI[dam-] bstYI/xholI mnlI afIIII acII alwI haellI/palI
1 CCAGGTCAA CTGCACTCG GTCATCGA TGAAATCC CGGGATCT CAGAGATCC CTCAGCCCG ACCACGGGT CGGCCAGCT GCCCTAGGA GACCTGGAC TGGTGCGA GGCGGTGCA CCCGGACGTG

xcmI
 scrPI [dcm-]
 pspGI [dcm-] bsrI sau96I [M.haeIII-]
 pspGI bsrI sau96I [M.haeIII-]
 mvaI haeIII/palI nlaIV
 ecORII [dcm-] haemIII/palI
 mvaI bspMI ddeI dsavI [dcm-] eco0169I/draII
 ecORII [dcm-] bspCNI nlaIV batNI eaeI mli
 dsavI [dcm-] mliI mliI basKI [dcm-] ddeI sau96I
 bstXI [M.haeIII-] hpy198III apyR [dcm-] bspCNI bsrI avail
 batNI eco8II banI mliI cfrI eco8II bsrI nlaIV
 bssKI [dcm-] bsu36I/mstII/sauI fnu4H/bsoFI bsu36I/mstII/sauI rmal
 fnu4H/bsoFI apyI [dcm+] haeIII/palI bsrI acII tspRI haeIII/palI maeI
 bsvI null haeIII/palI sau96I [M.haeIII-] bpaI/gsuI [dcm-] sau96I [M.haeIII-] bfaI
 :01 GGCTTGAGGG GAGGCTCTG TGGACAGGCC AGGCAGGTGG GCCTCAGGAG STGCCRCAG GCGGCCAGTG GCCTGAGG CCCATGAGG CCTTACGTCC
 CCGACGTTC CTCGAGAAC ACCCTCCGG TCCCTCCAC CGAGCTTC CACGAGTC CCGAGAAGC CGCCGTCAC CGCTGATCC CGATCCCAGG

bsp1286		scrFI(N.hpaII-)
nscl/balI	bryI	sau96I(dcm-)
scrFI [dcm-]		scrFI(dcm-)
pspGI	naII	pspGI nsPI
mva-	mvoI styI	mvaI hpaII
ecoriI(dcm-)	bgII [M.haeIII-] mvaI	ecoriI(dcm-)
dsaV [dcm-]	eae- ncov [M.haeIII-] mvoI	dsaV [dcm-]
bstNI	cfrI dsal	bstNI dsaV
bskI- [dcm-]	fnu4H- /bscFI	bskI [dcm-]
apyI (dcm+)	acII btgl/bstDST bstNI	bskI [dcm-]
bsmFI	nsPAlI/nsPBI haellI/pallI nlary	bskI [dcm-]
bsrl bsalI	tseI stIII bsalI	bskI [dcm-] fnu4H- /bscFI
bsll : dcm-]	bsalI	bsalI avail [dcm-] [M.hpaII-]
bpmI/gsuI (dcm-)	bbvI haellI/pallI bsl-	bbvI bsalI bsalI mvoI haellI/pallI
20 ATCTCCAGTC CCAAGACACC GCAACGGCCA CCTTGCCAC GCTGGGCTC CAGCACATC ACCACCCCC AGGACCGGG AGGCACAGGT GCCCCCACC TAGAGTCAG GGTCCTGTGT CGTCCGGGT GTTACGGTG CGGACCCGAC GTGGCTGTAG TCGTGGGGG TCCTGGCCC TCGTGTCCA CGGGGGTGG	nlary bsl	bsalI

Correct ORF^a

bceAI
haeIII/palI
mcRI
eagI/xmaRII/eclXI
eaEI
cfrI
bsI~~E~~I
msplI[M.haeIII-]
hpaII
scrFI-[M.hpaII-]
ncII
dsav
bspI
bmyI
banII hpy188III fnu4HI/bsoFI
mnlI bspCRI
bspI286 mwoI
bmyI ddeI mnlI tsEI
banII hpy188III fnu4HI/bsoFI
mnlI bspCRI
bspI286 mwoI
bSIKAI msplI[M.haeIII-]
btSI acII bmyI cfrI0I/bsrFI
GAGGGCTC CAGGAGCTC TGGTGTGTC GCTTGCTG TTGGAGTGC CGCGCACAGA GCACGCCATC CGCCCGGCC GTAGGGTGTG TGCCTGTCGG
CTGCCGAGA GTCCCTCACC ACCGACTACAC CGAAGACAC ACCGTCACT CGTGGGGAT CGCGGGCGG CATCCCAACAC ACGACAGGCC
23 E G L S G G A A D V A S G V G S G R H R A R L P A R P O
2 R G S Q R V L L W L L V L A V G G T E H A Y R P G R R V C A V R
deleted a T -goddarda [REDACTED]
deleted C -goddarda [REDACTED]

bsaXI

:th111/aspi

pflI

sau96-

r.larV

avall

tseI

scrFI [M.hpaII-]

ncII fnuMI/bsoFI

nsp- bbVI

hpaII hpyCH4V

r.larV cac8I

banI haell/pali

hpy99I dsav sfcI

hphi bslI bsp1286 sau96I [M.haeIII-]

bsMI bsrAI hincI bsgI capI nulI bspMI bmyI bssKI pstI [M.HI-]

bsII

501 acatcaccgg acccttcgtc cgaatgcgc ctccacggtg tgcacccccc cttccctcacc accctcgacc ggcacccggc ctgcggcacc tacggacca

cgactcccc TGGGACAGAG GCTCAACAG CACGTGGCAG ACATGCTGG GAGGAGTGG TGGACCTGC CGTGCCCCG GACGTGGAG AGGCTTGGI

35 A B G C P V S E S F V Q R V Y Q P F L T T C D G H R A C S T Y R T I



scrFI [dcm-]

pspGI

rval

ecoriI [dcm-]

pspGI

dsaV [dcm-]

pspGI

bstNI

ecoriI [dcm-]

pspGI

bskI [dcm-]

ecoriI [dcm-]

pspGI

GSeqEdit, DNA30943 [full], page 7

sau96

nlaIV

scrFI [dcm

pspGI

rval haeI

ecoriI [dc

pspGI

601 TCTATAGGAC CGCTTAACSC CCGAGCCCTG GACTGGCCC TGCCAGGCCT CGCTGCCGT GCTGGCCG CTGGAGACGG ACCGGGGC TTCCCTGGCC

69 Y R T A V R R S P G L A P A R P R Y A C C P G W K R T S . G L P G A

^edit R to C, does not change aa -goddarda [REDACTED]

tsel
 mwoI
 mmoi
 fnu4HI/bsoFI
 haellI/palI
 eaellI[dcm-]
 cfrI fnu4HI/bsoFI
 scrFI[dcm-] hpyCH4V
 pspGI bbvI tsel sfcI
 mval msplI/nspBII pstI
 ecORII[dcm-] fnu4HI/bsoFI
 dsavI[dcm-] bbvI ss8387I
 bstNI acil msplI/nspBII tsp45I
 b3sKII[dcm-] acII sbFI fckI acir maelliI
 apyI[dcm-] fnu4HI/bsoFI bstf5I hphiI
 bs
 701 CTGTGGAGCA GCAHALMGCC AGCCGCCATG CCGGAACGAA GGGAGCTGTC TCCACCTTGC CGCTTGCCG TGACACTTGCG
 GACACCTGT CGTATACGG TCGGGGTC GCCTGACAC AGGTGGACC GGGGACGGGG ACGGGACGC CTAACGCCCTTACGGCCCC ACTGTGAAAC
 102 C G A A I C Q P P C R N G G S C V Q P G R C R C P A G R R G D T C
 tsel alwNII[dcm-]
 fnu4HI/bsoFI msplI
 bbvI bpall nlav
 rnaII
 bsmI tsprI mnlI
 hinPI sfaNI nael/ngoMI bsrl
 fckI btsI maclI fnu4HI/bsoFI haellI hpyCH4V cac8I naeII
 hpy18I tsrf5I hpyCH4V bfaI acII bsmI afel/ecoriIII acII alw26I/bsmI bsII mnlI
 801 CACTCAGTG TGGATGAGTG CAGTCCTTGG AGGGCCGCT GTCCCCACCG CTCGCTCAC AGGGCCGCA GTCAGCTG CCACTGTTGG GAGGGCCACA
 GTCAGCTAC ACCTACTTAC GTCACCGATCC TCCCCGGCGA CAGGGTCGC GACCTAGTG TGGGGCCGCT CAATGACAC GGTCCACACC CTCCCCGTTG
 135 Q S D V D E C S A R R G G C P Q R C I N T A G S Y W C Q C W E G H S

scrF-[dcm-]	tseI	sa
pspG:	pspG	
fnu4H/bsoFI		
nvaI		
scrF-[dcm-]	scrF-[dcm-]	scrF
dsav[dcm-]	bbvI	bbvI
bstNI	hpyCH4V	hpyCH4V
sfc-	sau96I [M.haeIII-]	sau96I [M.haeIII-]
pstI[M.H1-]	haeIII/palI	haeIII/palI
tsel	nlaiV	nlaiV
fnu4H/bsoFI	pspGI	pspGI
fnu4H/bsoFI	cac8I	cac8I
sau96I	nvaI: bglI(M.haeIII-)	nvaI: bglI(M.haeIII-)
bbvI	bbvI	bbvI
bbvI	bbvI psuII[M.H1-]	bbvI psuII[M.H1-]
bslI	bsqI	bsqI
bserI	bstNI	bstNI
alul	alul	alul
M.pstI-]	alwNI [dcm-]	alwNI [dcm-]
cac8I	alwNI	alwNI
tspRI	alw26I	alw26I
bslI	bslI	bslI
bspI	bspI286	bspI286
avI	av	av
bspI	bspI	bspI
gsvI	gsvI	gsvI
[dcm-]	[dcm-]	[dcm-]
mspAII/nspRI	mspAII/nspRI	mspAII/nspRI
mlII hpyCH4V	mlII hpyCH4V	mlII hpyCH4V
100: GAGCTGCAG TCCAGGGGG ACCCTCTGA GGAGAACGTG GACCTGGTGC TGCCCCACT GCACGCCG GCCTCGCAGG CACTGGAGCA TGGCTTCG CTCCGACGCC AGGTCCACCC TGGAGGACCT CCTCTCGAC GTGAGCACCAG ACCGGGGTGA CGTGTTGGAC CGGAGGCTCC GTGACCTGCT ACCGGGGC 202 R L Q S R V D I L E E K L Q L V L A P L H S L A S Q A L E H G L P		

hgiA ⁻ /aspeI				
bspi286				
bsi3RAI				
bmyI				
scrF ⁻ [dcm-]				
teeI				
pspcI				
<i>fnu4HI/bsoFI</i>				
biv ⁻	<i>nval hpyCH4V</i>			
mspi	<i>ecoriI[dcm-]</i>			
hpaII	<i>dsavI[dcm-]</i>			
scrFI(M.hpaII-)	<i>apalI/snoI</i>			
ncI	<i>bsrKI</i>			
dsav	<i>bsKI[dcm-]</i>			
bssKI	<i>apyI[dcm-]</i>			
bsaCI	<i>mlI alw49I/snoI</i>			
110:	GACCCCGGCA GCTCTGGT GCACCTCTTC CACCGCTCG GCCCCATGA CTCCCTGAGC GACGAGATT CCTTCCTGGA GGAGCAGCTG GGCTCTGCT CTGGGGCGT CGAGGACCA CGTGAGGAGG GTCTCTGAGC CGCGTAGCT GAGGACTCG CTCGTCAA GGAGGACCT CCTCTGCGAC CCCGGACCA			
235	> 2 G S 2 L V H S F Q Q L G R I D S L S E Q I S P L E E Q L G S S C S			
		mLI		
		bseRI		
		bpml/gsul[dcm-]		
		scrFI[dcm-]		sau96I
		pspGI	tseI	avall
		nval	<i>fnu4HI/bsoFI</i>	
		ecoriI[dcm-]		pruMI
		dsavI[dcm-]	psuII[M.Ht-]	
		bsTI	bbVI	nlav
		bsSKI[dcm-]	alul	eccl09I/dr
		apyI[dcm+]	mspalI/bspBI	

scrFI[dcm-]							
pspGI							
aval							
ecoRII[dcm-]							
dsaV[dcm-]							
bstNI	mmol						
hpy88III	bs1I	bspl286					
bssSI	mwol	bsskI[dcm-]	bmyI				
p.IR tsP45I	hinfI	apyI[dcm+]	banII				
mlyI maelII	hhaI/cfoI	ddeI	actI	hpyCH4V			
hpaCH4V	hinE-	bsAI	PstI [M.HI-]	sfcI	nlairI	hpy1	
	↓	bsPcNI	mlII	smu111/bsoFI	bspHI	nsphi	sau36I
1201	ccTGCAAGCA AGACTCGTGA CTGCGCCGCC CCCAGGTG CACTGAGCC CTCACGCCCT CCTGAGGCC CCATGCCCT GCCCCATG CTGGGGTCC	nlairI	nlairI	tstXI	avaiI		
	GGACGCTCTT TCTGAGCACT GACGGGTGCC GGGTCCGAC CTGACTGGG GAGTGCAGG GGAAGTGGG GGTACGGGA CGGGTGTAC GACCCCCAGG	mwol	nsplI	nlairI			
263	C K D S O						

scrFI [dcm-]

papGI

nvaI

ecoRII [dcm-]

csaV [dcm-]

bstNI

bssKI [dcm-]

bslI [dcm-]

apyI [dcm+]

bsl-

bsaJI

alwNI [dcm-]

alm26I/bsmAI

fokI

bstF5I

bslI [dcm-]

nlairI

alwI

alw26I

bsmAI

fokI

bstF5I

bslI

nlairI

alwI

alw26I

bsmAI

fokI

1301 AGAGCCACC TCGGGCTGAC TGAAGGGAAAG CGCAGGGAGG GCCTTCCTCC TCTTCTCTCT CCCCCTCCCTC GGGAGGCTCC CGAGACCTG GCATGGGATG

TCTTCGGGG AGCCCCACTTG ACTTCGCTTC CGGTCCGTC CGGAGGGAGG AGAAGGAGGA CGGGAGGGAGG CCCCTCCAGG GTCCTGGGAC CGTACCCCTAC

^edit T to C -goddarda [REDACTED]

^deleted a C -goddarda [REDACTED]

edit G to C -goddarda [REDACTED]

sau96I [M.haeIII-]

haeIII/pali

sau96I [M.haeIII-]

pspOMI/bsp120I

nlaIV

bamI

asp718

scrFI [dcm-]

pspGI

sau36I

naiy

ava-I

sandi

ppjMI

nlaIV

mspI

eco01E9-/dratt

tseI bpall

scrFI[dcm-]

fnu4HI/bsoFI

pspC-

bbVI scrFI(M.hpaII-)

mvaI

pspGI

ncII

ecorRI[dcm-]

scrFI[dcm-]

dsav(dcm-)

mvaI dsav

bstXI

ecorRI[dcm-]

bsSI

bsav(dcm-)

bsaI

batNI

bsaI

bsaI

apyI(dcm+)

bsaI

maII
maI

maII

aluI

taeI

fnu4HI/bsoft

acc65-(GGTACCC):

sa

sa

s_cyI

s_cyI

tail

GSeqEdit, DNA30943 [Full], page 16

> _length: 1738

1447

DNA30943

The screenshot shows a software interface for gene annotation. At the top, there are tabs for 'GENE3DENES', 'SEARCH', 'FAIR MAP', 'CENTIMAP', 'SEQUENCE', 'SAS', 'RNA', 'LIP', 'FLS', 'COL', 'EXPERIMENTAL', 'COM', 'EXP', 'SUB', 'LOC', 'ASY'. Below these are buttons for 'SELECT' and 'REF'. On the right, there's a 'Find C New C Update' button and an 'Additional Resources' section with a 'MAP' link.

DNA30943

DNA Info Project DNA28735

Is Primary dna C

Source Info 187 FLS 339 LIP25 RNA22 SRC18 Human Fetal Lung

Gene Info PRO213 Human Egl17 (VEMF) Non-Secreted UNQ187

Gene Annotation

Genome Mapping Run Geode

Ally HGU133A 218825_at
HGU133P 218825_at
HGU95C 48695_at
Hu35KA R39467_f_at
Hu35KC RC_N74686_f_at
Hu35KD RC_N70081_at
HuGenen1 NM_016215_at
MOE430A 1421335_a_at, 1435823_x_at, 1451427_a_at, 1451428_x_at
MOE430P 1421335_a_at, 1435823_x_at, 1451427_a_at, 1451428_x_at
Rat230v2 1370402_at, 1374570_at, 1393427_s_at

Agilent H1Av2 A_23_P123785
H1A A_23_P123785
H1Av2 A_23_P123785
H1B A_32_P210642, A_32_P300230
M1A A_51_P315841
WHG A_32_P210642

FANTOM Mouse:0610012G11

Human:AB125849, AF186111, AL512735, AY358901, AY358902, AY358903, BC012377

GenBank Mouse:AE184973, AK002601, AY239259, AY239290, AY309459, BC024610

GeneHub Human:GENE7437
Mouse:MGENE1470

INCYFL Human:931424.FL1_0, 931424.FL3_0
Human:416842.1, 416842.13, 416842.17, 416842.56, 416842.58, 416842.62, 416842.64, 416842.67, 416842.68
Invitae 416842.69, 416842.70, 416842.72, 416842.74, 934053.1
Human:51162
Mouse:353158
MGI Mouse:2448923
OMIM Human:809582
Proteome Human:NP_958854.1
Mouse:NP_942017.1
RefSeq Human:NM_016215, NM_201446
Mouse:NM_178444, NM_198724, NM_198725
Unigene Human:hs.91481
Mouse:Mm.288933

General Info

Lab Name 28735.2

Insert Name undetermined

Generated By Full Length Screen

Type of DNA FLS

Insert ID Novel

Action Drp Not FL

Concentration

Origene Plate

Construct Info

Tag

Bases to Sequence

Insert (Digest) Size(bp) 1600

Reverse Size(bp) 1

Internal Size(bp) 239

Cut Size(bp)

Vector

Interest not reviewed

Origene CloneID

Origene Well

Exp System

Sequence Status

DNA30943

Antibody Info No antibody infoOther Info In Situ image available TaqMan Hit Transgenic Animal Model

Oligos	OLI5268	
	OLI5289	
	OLI5290	
	OLI5572	30943.f1
	OLI5573	30943.f2
	OLI7839	30943.tm.t1
	OLI7840	30943.tm.r1
	OLI7841	30943.tm.p1
	OLI7845	30943.tm.f3
	OLI7846	30943.tm.r3
	OLI7847	30943.tm.p3

Comments

Login	Date Entered	Annotation
dtb	[REDACTED]	homolog to an unknown human protein and to gass6. The mouse protein with 40 % identity clearly has a signal sequence whereas this clone does not. I think the clone is suspect.-ALG
goddarda	[REDACTED]	Sequencing in clone 64908 allowed us to correct three sequencing errors in 30943 which lie in the 5' UTR of the gene. However the presence of these errors caused us to identify the wrong 5' end of the ORF in the gene. -goddarda
goddarda	[REDACTED]	Sequence was flagged as poor quality during proofreading. Tried to rerun reactions with Big DYE chemistry, but too little DNA - signal unreadable. Requested more DNA [REDACTED] Never received -goddarda
goddarda	[REDACTED]	amplified colon tumors and to a lesser extent in lung tumors- TaqMan assay
jean	[REDACTED]	Clone 30943 from plasmid inventory plate is verified correct through partial sequencing

Legal Status No legal status

Status

Scientist Daryl Baldwin

Notebook 0

Page

Storage Location

Box

Slot

Inventory Status

Others Sent to pLASMID Archive
 Clone Verified

Date Entered [REDACTED]

Date Updated [REDACTED]

Date Completed

Date Canceled

Cancel Reason

Clone Status not reviewed

Sequence Status

Project Member

No Project member generated

FLS FLSDNA

No FLS, FLSDNA generated

Exp Construct

EXP	Lab Name	Construct DNA	System
EXP7559	Protein Engineering	DNA348527	Baculovirus

ABI

ABI Run.Lane Date Sequenced ABI Plate

ABI612.31 [REDACTED]

ABI612.32 [REDACTED]

ABI612.33 [REDACTED]

ABI612.34 [REDACTED]

ABI612.35 [REDACTED]

ABI612.36 [REDACTED]

ABI612.37 [REDACTED]

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ABI612.197 [REDACTED]

ABI612.198 [REDACTED]

ABI612.199 [REDACTED]

MA Plate

MA Plate

PLT129

Well Num

25

Well Location

C1

Date

08/11/1999

Type Plate

Inventory

Print Run

No Print run generated

XPT